```
                  *          20          *          40          *          60          *

exm1007  : ------VNUN-NNNEYELIIDSKNLSYPSNRNIIDHSRFPYTMNPNQPLQNTINYKEWLNMCQGMTQYGDNFETTAS :  67
cry1Aa   : ------------MDNNP---NINECLPYNCLSNPEVEVLGG---                                  :  26
cry1Ac   : ------------MDNNP---NINECLPYNCLSNPEVEVLGG---                                  :  26
cry11a   : --------MKLKNQDKHQSFSSNAKVD---KISTDS---LKNETDIELQNINHEDCLKMSEYEN              :  50
cry3Aa1  : MIRKGGRKGMNPANRSEHDTIKTTENNE---VPTNHVQYPLAETPNFILEDLNYKEFLRMTADNN------TE     :  63
cry3Ba   : MIRMGGRKGNPANRSEYDTIKTTENSE--LPTNHNQYPLADTPNSTLENYKEFLRMTADNS------TE        :  63
cry4Aa   : ---MNPYQNKNEYETLNASQKKLN--ISNNYTRYPIENSPKGLLQSTNYKDWLNMCQQNQQ------YGG        :  59
cry6Aa   : -------------                                                                :   -
cry7Aa   : ---------MNLNNLDGYEDSNR---TLNNSLNTPTQKALSPSLKNMNYQDFLSITEREQP---              :  49
cry8Aa   : ------MSPNNQNEYEIIDATPSTS---VSSDSNRYPFANEPTDAIQNMNYKDYLKMSGGENPEL--- FG       :  58
cry10Aa  : ---MNPYQNKNEYEIFNAPSNGFS---KSNNYSRYPLANKPNQPLKQNTINYKDWLNVCQDNQQYGNN------AG  :  62
cry16Aa  : ---MHYYGMRNEYDILNAASNNDS--NMSNTYPRYPLANPQQDLQMQNTINYKDWLNVCEGYHIENP------RE   :  61
cry19Ba  : ------MNSYQNKNEYEIILDAKRNTC--HMSNCYFKFYPLANDFQMYLRNTHYKDWIMMCEEASTAS---       :  58
cry24Aa  : ------MNUYQNKNEYELIESSQNNMN---MPNRYPFADDPNAVMKNGNYKDWVNECEGSN---              :  52


                  80          *          100          *          120          *          140          *

exm1007  : ADTIAAVSAGTIVSGTILAGIGGLTSISGPIGIICAIIISFGTLIIVFVPAGEUDKTVUTQFIKMGEIFVDTPLT  : 142
cry1Aa   : -ERIETGYTPIDISLSLTQFLISEF------VPGAGFVLGLVDIIWGIFGPSQ------WDAFPVQIEQLINQRIE  :  89
cry1Ac   : -ERIETGYTPIDISLSLTQFLISEF------VPGAGFVLGLVDIIWGIFGPSQ------WDAFLVQIEQLINQRIE  :  89
cry11a   : -VEPFVSASTIUTGIGIAGKILGTLG----VPFAGUVASLYSFLLGELGP-KG--KNUQUEIFMEHVEEIINQKIS  : 117
cry3Aa1  : ALDSSTTKDVIQKGISVVGQLLGVVG----FPFGGALVSFYTNFLNTIUPS------EDPUKAFMEQVEALMDQKIA : 130
cry3Ba   : VLDSSTVKDAVGTGISVVGQLLGVVG----VPFAGALTSFYQSFLNAIUPSD----ADPUKAFMAQVEVLIDEKIE  : 131
cry4Aa   : DFETFIDSGELSAYTIVWGTVTGFG----FTTPLGLALIGFGTILIPVLFPAQDQSN-TWSDFITUTKNIIKKEIA  : 130
cry6Aa   : -----------                                                                  :   -
cry7Aa   : -EALASCTAINTVVSVTGATLSALG----VPGASFITMFYLIKIAGLLLMPENG--KI-WDEFMIEVEALIDQKIE  : 116
cry8Aa   : NPETFISSTIUTGIGIVGRILGALG----VPFASQIASFYSFYVGQLLUPSKS--VDIUGEIMERVELVDQKIE    : 127
cry10Aa  : NFASSETTVGWSAGLIVVGTMLGAFA----APVLAAGIISFCTLLFIVGQSDPAN--VWQDLLNIGGRPIQEID    : 131
cry16Aa  : ASVRAGLGKGLGIVSTIVGFFGGS----IILDTIGLFYQISELLUPEDDTUQYTWGDIMNHVEDLIDKRIT       : 128
cry19Ba  : S---GPSQLFKVGGSIVAKILG------MIPEVGPLLSEWVSLFUFTIEEKNTVUEDMIKYVANLLKQLT        : 120
cry24Aa  : ----ISPSPAAAITSKIVSIVLKTLAKAVASSLADSIKSSLGISKVITENNVS------QVSNVQVHQILNRRIQ   : 117
```

FIG. 1A

```
              160         *         180         *         200         *         220
exmi007  : ESIKQLKLQTLEGFRQILQ-SYNTALDDWRKLKRLQAPGLPFSSALQQAALITLIKIRFNEVWHNDFIREIPGFGLE---  : 215
cryIAa   : EFARNQAISRLEGLSNLYQ-IYAESFREWEADPTN------------------PALREEMRIQFNDMNSALTTAIPLLAVQN---  : 152
cryIAc   : EFARNQAISRLEGLSNLYQ-IYAESFREWEADPTN------------------PALREEMRIQFNDMNSALTTAIPLLAVQN---  : 152
cryIIa   : TVARNKALTDLKGLGDALA-VHDSLESUVGMRNN------------TRARSVVKSQYIALELMFVQKLPSFAVSG---  : 180
cry3Aa1  : DYAKNKALAELQGLQNNVE-DVYSALSSVQQKNVSS------RNFHSQGRLRELFSQAESHFRNSMPSFAISG---  : 196
cry3Ba   : EYAKSKALAELQGLQNNFE-DVYNALDSUKKALPVHL------RSRSQDRLRELFSQAESHFRNSMPSFAVSG---  : 197
cry4Aa   : STYISNANKILNRSFNVIS-TYHNHLKTWENNPN------------PQNTODVKTIQLVHVHFQNVIPELVNSCPPN    : 195
cry6Aa   :                                                                                     : -
cry7Aa   : EYVNRKAIAELDGLGSALD-KYUKALADWLGKQDD------------PEAILSVAITFRIIDSLFFFSMPSFKVTG---  : 179
cry8Aa   : KYVRDKALAELAKGLNWALD-VTQQSLEDULENRND------ARTRSVVSNQFIALDLMFVSSIFSFAVSG---  : 190
cry10Aa  : KNIINVLTSIVTPIKNQLD-KYQEFFDKWKPARTH------AMAKAVHDLFTTLEPIIDKDLDMLKNNAS---  : 194
cry16Aa  : EVIRGNAIRTLADIQGKFD-DYNNWLKKWKODP------KSTGNLSTIVTKTTALDSDFNGALRTVNNQGSP---  : 193
cry19Ba  : NDTLNRATSNLSGLNESLN-IYNRALIAAWKQNK------NNFASGELIRSYINDLHILFTRDIQSDFSLG---  : 183
cry24Aa  : ETIIDLGESSLNGLVAIYARDYLGLAFAUNNNKSN------INYUTNVAFAFKTVEREFFTKLKGLYRTSS---  : 182


              240         *         260         *         280         *         300
exmi007  : ----TYKTLLPIYAQAANTHLNLLQQGAELADEUNADIHPSQIEFNAGTSDDYYK-LLKEMIPKYSNYCANTY  : 284
cryIAa   : ----YDVPLLSVYVQAANLHLSVLRDVSVFG---------QRUGFDAATINSRYN-DLTRLIGNVTDYAVRGV  : 211
cryIAc   : ----YDVPLLSVYVQAANLHLSVLRDVSVFG---------QRUGFDAATINSRYN-DLTRLIGNVTDYAVRGV  : 211
cryIIa   : ----EEVPLLFIYAQAANLHLLLRDASIFG---------KEUGLSSSEISTFYN-RQVERAGDVSDHCVKGV  : 239
cry3Aa1  : ----YEVLFITYAQAANTHLFLLKDAQLYG---------EEUGYEKEDIAEFYK-RQLKLTUEYTDHCVKGV  : 255
cry3Ba   : ----FEVLFLFTYAQAANTHLLLLKDAQVFG---------EEUGYSSEDIAEFYQ-RQLKLTUQYTDHCVNUY  : 256
cry4Aa   : FSDCDDYNILVLSSYAOAANIHITVLNQUAVKFEAYLKQN-RQPDYLEFLFLAIDYYP-VLTKAIEDYTNYCVTTY  : 268
cry6Aa   : ---MIDSKTTLPRHSLIHTIKLNSNKKYG---------------PGDMTNGNQ--FIISKDQEWATIGAYL  : 51
cry7Aa   : ----YEIPLLTVYAQAANLHLALLRDSTLYG---------DKUGFTUNNIEENYN-RQKKRLSEYSDHCTKGV  : 238
cry8Aa   : ----HEVLLAVYAQAVNLHLLLRDASIFG---------EEUGFTPGEISRFYN-RQVOLTAEYSDYCVKGV  : 249
cry10Aa  : ----YRLPTLPAYAQIATUELNLKHAATYYNLUN----QGINFSTFNSSNYYQGYLKRKLUEYTDYCIQTY  : 260
cry16Aa  : ----GYELLLPVYAQIANLHLLLRDAQIYGD---------KUWSARAWARDNYYQ-IQLEKTKEYTEYCLNUY  : 254
cry19Ba  : ----GYEIVLSPYSASAANLHLLLRDVALYG---------KELGYPSTDVEFYYN-EQKYYIEKYSNYCVNTY  : 243
cry24Aa  : ----SQITLLPTFTQAANLHLSMLRDAVMYQEG------UNLQSHINVSKELDDALEDYTNYCVEVY  : 239
```

FIG. 1B

```
                  *        320        *        340        *        360        *
exmi007 : REGLNKLKNEPN-------MR-WSIFNDYKRYMTIITVLDTIAQFSFYDIKRVKDSIG--RIGGIKTELTRELYITTEI : 351
cry1Aa  : NTGLERVGGPD--------SRDWVRYNQFRRELITLVLDIVALFSNYDSRRYP----------IRTVSQLTREIYTNPV  : 272
cry1Ac  : NTGLERVGGPD--------SRDWVRYNQFRRELITLVLDIVALFPNYDSRRYP----------IRTVSQLTREIYTNVN  : 272
cry1Ia  : STGLANLRGTN--------AESWVRYNQFRRDMTLMVLDLVALFPSYDTURYP----------IKTTAQLTREVYTDAI  : 300
cry3Aa1 : NVGLDKLRGSS--------YESWVNFNRYRRELTLTVLDLIALFPLYDVRLYP----------KEVKTELTRDVLTDPI  : 316
cry3Ba  : NVGLNSLRGST--------YDAVVKFNRFRRELTLTVLDLIVLFPFYDVRLYS----------KGVKTELTDIFTDPI   : 317
cry4Aa  : KKGLNLLKTTPDSNLDGINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYP------------IGVQSELTREIYVQLN  : 335
cry6Aa  : QTGLGLPVWEQ--------QLRTHVNLSQDISIPSDFSQLYDVYCSDKT5------------A-FWGNKNLYPLII    : 106
cry7Aa  : NSGLSRLNGST--------YEQWINYHFRREMIMALDIVAVFPFHDPRRYS-----------METSTQLTREVYTDFV  : 299
cry8Aa  : KIGLDKLKGTI--------SKSWLNYHQFRREMTLLVLDIVALFPNYDTHMYP---------IETTAQLTRDVYTDPI  : 310
cry10Aa : NAGLTMIRINTN-------ATWNMYNTYALEMTIVLDLLAIFPNYDPEKYP-----------IGVKSELIREVYVTNVN : 321
cry16Aa : NKGLNDFRTAG--------QUVWFMRYRREMTLTVLDIISMFPIYDARLYP-----------TEVKTELTREIYSDVI  : 313
cry19Ba : KSGLESKKQIG--------WSDFNRYRREMTLSVLDIVALFPLYDTGLYPSKDG--------KIHVKAELTREIYSDVI : 306
cry24Aa : TKGLNALRGST--------AIDVLEFNSFRRDMTLMVLDIVALFPFNYAVPVRYP-------LSTKISLSRKLYIDPV  : 300

              *        380         *        400         *        420         *        440
exmi007 : NFDRLIYTLEIQFN----------LAIMEYNLIRSGLRLFSFLDELIFYTKWETYGNRLVGIANRNRSTYAT------TG : 414
cry1Aa  : LENFDGSFRG-----------MAORIEQNIRQ-PHLMDLNSITIYTDVHRGFNYVSGHQITASPVGFSGP--EF       : 333
cry1Ac  : LENFDGSFRG-----------SAOGIERSIRS-PHLMDILNSITIYTDAHRGYYVSGHQIMASPVGFSGP--EF       : 333
cry1Ia  : GTVEHPSFTSTTWYANNAPSFSAILEAAVVNN-PHLLDFLEQVTIYSLLS-----RWSNTQYNNWGGH--KL         : 365
cry3Aa1 : VGVNNLRGYG-----------TTFSNIENYIRK-PHLYDYLHRIQFHTRFQ----GYYGNDSFNYWSGNYVST        : 374
cry3Ba  : FTLNALQEYG-----------PTFSSIENSIRK-PHLFDYLRGIEFHTRLRP---GYSGKDSFNYWSGNYVET        : 375
cry4Aa  : FEESPYKYYD-----------FQVGEDSLTRPPHLFTWLDSLNFYEKAQTTPNNFTSRYMHYTLDNIS--Q          : 396
cry6Aa  : KSANDIASYG-----------FKVAGDPSIKKDGYFKKLIQKDELEDNIVDMNSDDDAIAKAIKDFKARCGIIIKEAK   : 170
cry7Aa  : SLSISNPDIGP----------SFSQMENTAIRT-PHLVDYLDELYIYTSKYKAFSEIQPDLFYUSAHKVS----F      : 360
cry8Aa  : AFNLVTSTGCNFWSTHSGLLFYEVENNVIRP-PHLFDILSSVELITSRGG----I-TLNNDAYINYWSGH--TL       : 377
cry10Aa : SDTFKITTELENG--------LITRN----------PTLFTWINQGRFYTRNSR----DILDYDIFSTTGNQMAF      : 374
cry16Aa : NGEIYGLMTPYFS--------FEKAESLYTRA-PHLFTWLKGFRFVTNSISVGTFLSGGQNKYSTNNS-S--IN       : 376
cry19Ba : NDHVYGLMPYYIS--------FEHAFSLYTR-PHAFTWLKGFRFVTNSINSUTFLSGGENRYFLITHGET--IY       : 370
cry24Aa : GRTDSFSFGDWTNIG----RTLANFNDRLEREVTDSFSPSLVWKULGDMTIYTGAIDSYRFTSFGDRIGVVYGNINAFYHT : 373
```

FIG. 1C

```
                       *          620         *          640         *          660         *
exmi007   : KIITMIPAIKGMSLDTNSKVYIEGPCHTCGNLVYLQSQG--------RLEITTCRTPWSTQSYYIRLRYATNGAGNTL : 626
cry1Ac    : SQTTQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPG---------QISTLRVNITAPLSQRYRVRIRYASTTNLQFH : 537
cry1Ac    : DSTTQIPAVKGMFLFNGSVIS-GPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLN : 542
cry1Ie    : NSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG--------TFGDIRVMINPPAQRYRVRIRYASTTDLQFH : 574
cry3Aa1   : KKITQLPLVKAYKLQSGASVSAGPRFTGGDIIQCTE---------MGSAATIVYTPDVSYSQKYRARIRYASTSQITTT : 584
cry3Ba    : EKITLPVVKAYALSSGASIIEGPGFTGGNLLFLKESS-----NSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLF : 589
cry4Aa    : HLTTUIPAVKANSLGTASKVVQGPGHTGGDLIDFKD---------HFKITCQHSWFQGSYFIRLRYASNGSANTR : 601
cry6Aa    : EAIKVFQKLQGIWATIGAQIEWLRTTSLQEVQDSDDADEIQIELEDASDAWLVVAQEARDFTLNAYSTNSRQNLP : 394
cry7Aa    : NKITKLPAVKMYKLDDPSTVVKGPGFTGGDLVKRGSTG--------YIGDIKATVNSPLSQKYRVRVRYATANVSGQFN : 564
cry9Ba    : DKITQIPAVKGMDMLYLGGSVVQGPGFTGGDILKRINPS--------ILGTFAVTVNGSLSQRYRVRIRYASTTDFEFT : 593
cry10Aa   : DWITQIHALKALKVSSDSKIVKGPGHTGGDLVTLKDS---------MDFRVRFLKNVSRQYQVRIRYATNAPKTIV : 574
cry16Aa   : NKITQIPVVKASSINGSISIEKGPGFTGGDLVKMRADS--------GLTHRFKAELLDKKYRVRIRYKCNYSSKLI : 577
cry19Ba   : DKIVUIPAVKTMLVGANIIK--GPGHTGGDLLKLEYER---------FLSLRIK-LIASMTFRLRIRYASNISGDQM : 568
cry24Aa   : DEITQIPAVTAYELRGNSSVVAGPGSTGGDLVKMSYHS--------VUSFKVYCSELKNVRVRIRYASHGNCQFL : 579
```

```
             680         *          700         *          720         *          740         *
exmi007   : PNISILTIPGVIGIPPQRLNNTFSGTNYN-NLQYGDFGYFQFPSTVTLPLMR---NIPFIFNRADVSN-SILLIDKI : 697
cry1Ac    : TSIDG--------RPINQGNFSATHSSGSS---NLQSGSFRTVGFTTPFNFSNG---SSVTLSAHVFNSGNEVYIDRI : 601
cry1Ac    : VNWGN--------SSIFSNTVPATATSLD---NLQSDDFEVFESANAFTSSLG----N---IVGVRNFSGTAGVIIDRF : 603
cry1Ie    : TSING--------KAIDGQNFSATNRGE----DLDYKTFRTVGFTTPFSLDV----QSTTIGAVNFSSGNEVYIDRI : 638
cry3Aa1   : LSLDG--------APFNQYYFDKTINKGD----TLTYNSFNLASFSTPFELSG----NNLQIGVTGLSAGDKVYIDRI : 646
cry3Ba    : VQNSN--------NDFLVIYINKTMIDG----DLIYQTFDFATSNMGFSGD----TNDFIIGAESFVSNEKIYIDKI : 653
cry4Aa    : AVINLSIPG--VAEILGMALNFTFSGTDYTNLKYKDFQYLEFSMEVKFAFNQ---NISLVFNRSDVYINTTVLIDKI : 672
cry6Aa    : INVISDCNCSTTNMTSNQYSNPTTNMTSNQYMILSHEYTSLPNNFMLSRN----SNLEYRCPENNFMLRYVNNS : 674
cry7Aa    : VYIND--------KITLQTKFQNTVETIGEKGDLTYCSFCYLEYSTTIQFPDE---HPKITHLSDLSNNSSFYVDSI : 631
cry9Ba    : VIND--------RPINQEMFTKHDNGA----SLTYETFKFASFITDFQFET----QDKILLSMGDFSSGQEVYIDRI : 656
cry10Aa   : FLTG--------DTTSVELPSTTSRQNPNATDLTYADFGYVTFRTVPNKTFEEDTLMTLVGTPMNSYIYIDRI : 644
cry16Aa   : LRKUKGE-----GYIQQLENISPTYG----AFSYLESFTITTIENIFDLTM---EVTYPGRQFWEDIPSLLIDKI : 642
cry19Ba   : INIUG--------YQNPTYFNIIPTTSRD-YTELKEPDFOLVDTSYIYSGGP---SISSNTIWLDNFSNGPVIIDKI : 632
cry24Aa   : MKRUFS--------TGVAPRQUARHNVQGTFSNSMRYEAFKYLDIFITTPEENN----------FAFTIDLESGGDLIFDKI : 643
```

FIG. 1D

```
                760         *         780         *         800
exmi1007 : EFIPITSSVRQMRE---KQKLETIQTKINTFFTMHTKNTLMIEAITNYDID : 744
cry1Aa   : EFVPAEVTFEAEYD---LERAQKAVNELFTSSNVIGLKTDVTDYHIDQVS : 648
cry1Ac   : EFIPVTATLEAEYN---LERAQKAVNALFTSTNVLGLKTNVTDYHIDQVS : 650
cry1Ia   : EFVPVEVTYEAEYD---FEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVS : 685
cry3Aa1  : EFIPVN------------------------------------------- : 652
cry3Ba   : EFIPVQ------------------------------------------- : 659
cry4Aa   : EFLPITRSIREDREKQKLETVQQIINTFYANPIKNTLQSELTDYDIDQAA : 722
cry6Aa   : DUYNNSDUYNN--------------------------------------- : 475
cry7Aa   : EFIPVDVNYAEKEK---LEKAQKAVNTLFTE-GRNALQKDVTDYDYKVDQVS : 677
cry9Aa   : EFIPVDETYEAEQD---LEAAKKAVNALFTNTKD-GLRPGVTDYEVNQAA : 702
cry10Aa  : EFIPITQSVLDYTEKQNIEKTQKIVNDLFVN------------------- : 675
cry16Aa  : EFLPTN-------------------------------------------- : 648
cry19Ba  : EFIPLGITLNDAQG---YDTYDQNANGMYHQNYSNSGYNYNQEYNTYYQS : 679
cry24Aa  : EFIPVSGSAFEYECKQNIEKTQKAVNDLFIN------------------- : 674
```

FIG. 1E